



SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the Secretary, Department of Health and Human Services, c/o Centers for Disease Control and Prevention Chang, Gwong-Jen J.

<120> NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION

<130> 6395-64908

<150> PCT/US02/10764

<151> 2002-04-04

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

<160> 61

<170> PatentIn version 3.2

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NOV 07 2003

TECH CENTER 1600/2900

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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro			
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Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu			
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Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val			
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Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn			
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Gly Cys Gly Leu Phe Gly Lys Ser Ile Asp Thr Cys Ala Lys Phe			
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Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile			
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Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn			
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Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu			
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Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg			
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Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala			
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Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His			
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Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys			
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tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct			2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala			
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Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser			
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Phe Val Ala Thr Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu			
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ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag			2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln			
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atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt			2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe			
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Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr			
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Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys			
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 35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
 50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
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Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
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Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
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Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260 265 270

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Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
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Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
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Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335

Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350

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355 360 365

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370 375 380

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Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
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His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
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Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
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<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> MISC_FEATURE
<223> JE Signal

<400> 14

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala
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<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
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<222> (1)..(5308)
<223> pCBWN

<220>
<221> CDS
<222> (911)..(2986)

<400> 15
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cgagcaaaat ttaagctaca acaaggcaag gcttaccga caattgcatt aagaatctgc	180
ttagggtagtgcg ctgcttcgcg atgtacgggc cagatatacg cggtgacatt	240
gattatttgc tagttattaa tagtaatcaa ttacgggtc attagttcat agccatata	300
tggagttccg cgttacataa cttacggtaa atggccgc tggctgaccg cccaaacgacc	360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggacttcc	420
attgacgtca atgggtggag tatttacggt aaactgccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
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tcgctattac catggtgatg cggttttgg cagtagatca atggcgtgg atagcggtt	660
gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gtttggcac	720
caaaatcaac gggacttcc aaaatgtcgt aacaactccg ccccattgac gcaaatggc	780
ggtaggcgtg tacggtgga ggtctatata agcagagctc tctggctaac tagagaaccc	840
actgcttact ggcttatcga aattaatacg actcactata gggagaccca agcttggta	900
cgccgcccgc atg ggc aag agg tcc ggc tca atc atg tgg ctc gcg	949
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala	
1 5 10	
agc ttg gca gtt gtc ata gct tgg gca ggc gcc gtg acc ctc tcg aac	997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn	
15 20 25	
ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat	1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp	
30 35 40 45	
gtc atc acg att cca aca gct ggt gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
50 55 60	
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
65 70 75	
cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
80 85 90	
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	

agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala 130 135 140	1333
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly 145 150 155	1381
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr 160 165 170	1429
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct Met Gln Arg Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala 175 180 185	1477
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly 190 195 200 205	1525
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys 210 215 220	1573
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met 225 230 235	1621
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu 240 245 250	1669
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly 255 260 265	1717
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln 270 275 280 285	1765
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys 290 295 300	1813
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile 305 310 315	1861
gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe 320 325 330	1909
gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln 335 340 345	1957
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro 350 355 360 365	2005

tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys 370 375 380	2053
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val 385 390 395	2101
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn 400 405 410	2149
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr 415 420 425	2197
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala 430 435 440 445	2245
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile 450 455 460	2293
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu 465 470 475	2341
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr 480 485 490	2389
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr 495 500 505	2437
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly 510 515 520 525	2485
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr 530 535 540	2533
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr 545 550 555	2581
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser 560 565 570	2629
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His 575 580 585	2677
aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Leu Lys Gly 590 595 600 605	2725

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cctatctcag	cgatctgtct	attcgttca	tccatagttg	cctgactccc	cgtcgtgtag	4396
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tcattctgag	aatagtgtat	gcggcgaccg	agttgctctt	gccggcggtc	aatacgggat	4936
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ttccttttc	aatattatttgc	aagcatttat	cagggttatt	gtctcatgag	cggatacata	5236
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<210> 16
 <211> 692
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct
 <400> 16

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 20 25 30

Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
35 40 45

Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
50 55 60

Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
85 90 95

Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115 120 125

Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130 135 140

Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
165 170 175

Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
195 200 205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
210 215 220

Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225 230 235 240

Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
245 250 255

Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
260 265 270

Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
290 295 300

Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
305 310 315 320

Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
325 330 335

Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
340 345 350

Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
355 360 365

Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
370 375 380

Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
385 390 395 400

Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
405 410 415

Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
435 440 445

Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
450 455 460

Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
465 470 475 480

Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
485 490 495

Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
500 505 510

Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
515 520 525

Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
530 535 540

Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545 550 555 560

Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
580 585 590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
595 600 605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
610 615 620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
660 665 670

Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
675 680 685

Asn Val His Ala
690

<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature

<222> (1)..(5334)

<223> pCBJE 1-14

<220>

<221> CDS

<222> (916)..(3006)

<400> 17

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180										
ttagggttag	gcgtttgcg	ctgcttcg	atgtacggc	cagatatacg	cgttgacatt	240										
gattattgac	tagttattaa	tagtaatcaa	ttacgggtc	attagttcat	agccatata	300										
tggagttccg	cgttacataa	cttacggtaa	atggccgc	tggctgaccg	cccaacgacc	360										
cccgcccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420										
attgacgtca	atgggtggag	tat	ttacgggt	aaactgccc	cttggcagta	catcaagtgt	480									
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tcgctattac	catggtgatg	cgggttggc	agtacatcaa	tggcgtgga	tagcggttg	660										
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tggagtttgc	ttttggcacc	720										
aaaatcaacg	ggactttcca	aatgtcgta	acaactccgc	cccattgacg	caaatggcgc	780										
gtaggcgtgt	acgggtggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840										
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900										
tctagagccg	ccgccc	atg	ggc	aga	aag	caa	aac	aaa	aga	gga	aat	gaa	951			
		Met	Gly	Arg	Lys	Gln	Asn	Lys	Arg	Gly	Gly	Asn	Glu			
		1					5					10				
ggc	tca	atc	atg	tgg	ctc	g	gc	ag	tt	g	ca	gt	tgc	999		
Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala	Val	Val	Ile	Ala	Cys	Ala	
15							20					25				
gga	gcc	atg	aag	ttg	tgc	aat	ttc	cag	ggg	aag	ctt	ttg	atg	acc	atc	1047
Gly	Ala	Met	Lys	Leu	Ser	Asn	Phe	Gln	Gly	Lys	Leu	Leu	Met	Thr	Ile	
30							35					40				
aac	aac	acg	att	gca	gac	gtt	atc	gtg	att	ccc	acc	tca	aaa	gga	1095	
Asn	Asn	Thr	Asp	Ile	Ala	Asp	Val	Ile	Val	Ile	Pro	Thr	Ser	Lys	Gly	
45							50			55		60				
gag	aac	aga	tgc	tgg	gtc	cg	gca	atc	gac	gtc	ggc	tac	atg	tgt	gag	1143
Glu	Asn	Arg	Cys	Trp	Val	Arg	Ala	Ile	Asp	Val	Gly	Tyr	Met	Cys	Glu	
65										70		75				
gac	act	atc	acg	tac	gaa	tgt	cct	aag	ctt	acc	atg	ggc	aat	gat	cca	1191
Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	

80	85	90	
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr 95 100 105 1239			1239
gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val 110 115 120 1287			1287
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala 125 130 135 140 1335			1335
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn 145 150 155 1383			1383
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly 160 165 170 1431			1431
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu 175 180 185 1479			1479
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly 190 195 200 1527			1527
aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu 205 210 215 220 1575			1575
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro 225 230 235 1623			1623
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu 240 245 250 1671			1671
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val 255 260 265 1719			1719
gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp 270 275 280 1767			1767
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300 1815			1815
gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe 305 310 315 1863			1863
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile			1911

320	325	330	
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn 335	340	345	1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350	355	360	2007
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr 365	370	375	2055
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu 385	390	395	2103
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400	405	410	2151
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr 415	420	425	2199
gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala 430	435	440	2247
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Leu His 445	450	455	2295
cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Val Lys 465	470	475	2343
tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480	485	490	2391
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495	500	505	2439
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510	515	520	2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525	530	535	2535
agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545	550	555	2583
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu			2631

560	565	570	
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln 575 580 585			2679
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe 590 595 600			2727
tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605 610 615 620			2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635			2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650			2871
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655 660 665			2919
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr 670 675 680			2967
ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taatttagtt Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala 685 690 695			3016
gagcggccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag			3076
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ggttattgtc	tcatgagcgg	atacatattt	gaatgtatTT	agaaaaataa	acaaataggg	5296
gttccgcgca	cattttcccg	aaaagtgcac	cctgacgt			5334

<210> 18
 <211> 697
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 18

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
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Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val

225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260 265 270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
275 280 285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
290 295 300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305 310 315 320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325 330 335

Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr
340 345 350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
355 360 365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
370 375 380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
385 390 395 400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
420 425 430

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
435 440 445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
450 455 460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly

465

470

475

480

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
485 490 495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
500 505 510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
515 520 525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
530 535 540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545 550 555 560

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
565 570 575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625 630 635 640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
645 650 655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
660 665 670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
675 680 685

Val Phe Leu Ala Thr Asn Val His Ala
690 695

<211> 5283
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> CDS
 <222> (910)..(2964)

 <400> 19

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ccgcata	aggcagtat	ctgctccctg	cttgtgtgtt	ggaggtcgct	gagtagtgcg	120										
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180										
ttagggtag	gcgtttgcg	ctgcttcg	atgtacgggc	cagatatacg	cgttgacatt	240										
gattattgac	tagtattaa	tagtaatcaa	ttacgggtc	attagttcat	agccatata	300										
tggagttccg	cgttacataa	cttacggtaa	atggcccgcc	tggctgaccg	cccaacgacc	360										
cccgcccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420										
attgacgtca	atgggtggac	tat	ttacgggt	aaactgccc	cttggcagta	480										
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taatggccc	gcctggcatt	540										
atgcccagta	catgacctta	tggactt	ctacttggca	gtacatctac	gtattagtca	600										
tcgctattac	catggtgatg	cggtttggc	agtacatcaa	tggcgtgga	tagcggtt	660										
actcacgggg	atttcca	atgtccca	ttgacgtcaa	tggagttt	tttggcacc	720										
aaaatcaacg	ggactttcca	aatgtcgta	acaactccgc	cccattgacg	caaatggcg	780										
gtaggcgtgt	acgggtggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840										
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900										
gccggccgc	atg	ggc	aag	agg	tcc	951										
Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser			
1	5	10														
ttg	gca	gtt	gtc	ata	gct	ggt	aca	agc	gct	acc	acc	atc	cac	cg	gac	999
Leu	Ala	Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Thr	Thr	Ile	His	Arg	Asp	
15		20					25					30				
agg	gaa	gga	tac	atg	gtt	atg	cg	gcc	agt	gga	agg	gac	gct	gca	agc	1047
Arg	Glu	Gly	Tyr	Met	Val	Met	Arg	Ala	Ser	Gly	Arg	Asp	Ala	Ala	Ser	
35							40					45				
cag	gtc	agg	gta	caa	aac	gga	acg	tgc	gtc	atc	ctg	gca	aca	gac	atg	1095
Gln	Val	Arg	Val	Gln	Asn	Gly	Thr	Cys	Val	Ile	Leu	Ala	Thr	Asp	Met	
50				55						60						
gga	gag	tgg	tgt	gaa	gat	tca	atc	acc	tac	tct	tgc	gtc	acg	att	gac	1143

Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp			
65	70	75	
cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat			1191
Gln Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp			
80	85	90	
agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg			1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg			
95	100	105	110
ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc			1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val			
115	120	125	
ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc			1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val			
130	135	140	
acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc			1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala			
145	150	155	
att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg			1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val			
160	165	170	
act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg			1479
Thr Val Ile Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg			
175	180	185	190
tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc			1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr			
195	200	205	
acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca			1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr			
210	215	220	
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag			1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln			
225	230	235	
gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc			1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr			
240	245	250	
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt			1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu			
255	260	265	270
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac			1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp			
275	280	285	
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg			1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val			
290	295	300	
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac			1863

Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His			
305	310	315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac			1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His			
320	325	330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca			1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser			
335	340	345	350
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac			2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp			
355	360	365	
tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc			2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val			
370	375	380	
gcc caa act gtg gtg atg tca ctc gac agc aag gac cac ctg cct			2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro			
385	390	395	
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc			2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro			
400	405	410	
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg			2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val			
415	420	425	430
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg			2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly			
435	440	445	
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc			2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala			
450	455	460	
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt			2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys			
465	470	475	
gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg			2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met			
480	485	490	
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc			2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly			
495	500	505	510
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca			2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro			
515	520	525	
tgt cgg atc ccg gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat			2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn			
530	535	540	
gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc			2583

Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly		
545	550	555
gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg		2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val		
560	565	570
gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga		2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg		
575	580	585
atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga		2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly		
595	600	605
gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg		2775
Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val		
610	615	620
ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt		2823
Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe		
625	630	635
ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc		2871
Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val		
640	645	650
tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt		2919
Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu		
655	660	665
670		
gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca		2964
Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala		
675	680	685
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gcggtagct	ccttcggtcc	tccgatcg	gtcagaagta	agttggccgc	agtgttatca	4764
ctcatggta	tggcagca	gcataattct	cttactgtca	tgccatccgt	aagatgctt	4824
tctgtgactg	gtgagtagtc	aaccaagtca	ttctgagaat	agtgtatgc当地	gcgaccgagt	4884
tgctcttgcc	cggcgtaat	acggataat	accgcgccac	atagcagaac	tttaaaagtg	4944
ctcatcattg	gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	gctgttgaga	5004
tccagttcga	tgttaacccac	tcgtgcaccc	aactgatctt	cagcatctt当地	tactttcacc	5064
agcgttctg	ggtgagcaaa	aacaggaagg	caaaatgccg	caaaaaaggg	aataagggcg	5124
acacggaaat	gttgaatact	catactcttc	cttttcaat	attattgaag	catttatcag	5184
ggttattgtc	tcatgagcgg	atacatat	aatgtattt	agaaaaataa	acaaataggg	5244
gttcccgca	catttccccg	aaaagtgc当地	cctgacg	tc		5283

<210> 20
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 20

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp Arg Glu
20 25 30

Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser Gln Val
35 40 45

Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu
50 55 60

Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu
65 70 75 80

Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp Arg Val
85 90 95

Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys
100 105 110

Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg
115 120 125

Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg
130 135 140

Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val
145 150 155 160

Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val
165 170 175

Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr
180 185 190

His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg
195 200 205

Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr Ala Glu
210 215 220

Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser
225 230 235 240

Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr
245 250 255

Lys Val²⁶⁰ Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu
265 270

Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly
275 280 285

Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr
305 310 315 320

Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly
325 330 335

Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln
340 345 350

Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly
355 360 365

Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln
370 375 380

Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala
385 390 395 400

Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys
405 410 415

His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe
420 425 430

Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln
435 440 445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val
450 455 460

Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val
465 470 475 480

Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met Cys Asp
485 490 495

Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp
500 505 510

Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg
515 520 525

Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala
530 535 540

Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Phe
545 550 555 560

Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp
565 570 575

Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe
580 585 590

Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His
595 600 605

Ala Trp Asp Phe Gly Ser Val Gly Val Leu Ser Ser Val Gly Lys
610 615 620

Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly
625 630 635 640

Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu
645 650 655

Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu Ala Val
660 665 670

Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala
675 680 685

<210> 21
<211> 5304
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2985)

<400> 21

gacggatcgg gagatctccc gatcccstat ggtcgactct cagtacaatc tgctctgatg 60

ccgcatagtt aagccagttat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180

ttagggtagtgcg ctgcttcgct atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360

cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggac tatttacgtt aaactgccc a cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgaccccta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggtttggc agtacatcaa tggcgtgga tagcggttg 660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagttt ttttggcacc 720

aaaatcaacg ggactttcca aatgtcgta acaactccgc cccattgacg caaatggcg 780

gtaggcgtgt acggtggag gtctatataa gcagagctct ctggctaact agagaaccca 840

ctgcttactg gcttatcgaa attaatacga ctcactatacg ggagacccaa gcttggtacc 900

gccgcccccc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat 999

Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
15 20 25 30

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc 1047

Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
35 40 45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct 1095

Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
50 55 60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca 1143

Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
65 70 75

gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp 80 85 90	1191
gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His 95 100 105 110	1239
tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser 115 120 125	1287
aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc acc Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr 130 135 140	1335
aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr 145 150 155	1383
gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr 160 165 170	1431
cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr 175 180 185 190	1479
agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala 195 200 205	1527
agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Ser Cys Val 210 215 220	1575
aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys 225 230 235	1623
atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala 240 245 250	1671
acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu 255 260 265 270	1719
gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp 275 280 285	1767
gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly 290 295 300	1815
agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly 305 310 315	1863

aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val 320 325 330	1911
cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile 335 340 345 350	1959
gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser 355 360 365	2007
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu 370 375 380	2055
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys 385 390 395	2103
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu 400 405 410	2151
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu 415 420 425 430	2199
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta Val Glu Phe Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu 435 440 445	2247
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro 450 455 460	2295
gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa Ala Thr Val Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys 465 470 475	2343
tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly 480 485 490	2391
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly 495 500 505 510	2439
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro 515 520 525	2487
tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro 530 535 540	2535
gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala 545 550 555	2583

aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr 560 565 570	2631
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys 575 580 585 590	2679
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala 595 600 605	2727
caa cg ^g cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile 610 615 620	2775
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly 625 630 635	2823
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly 640 645 650	2871
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg Leu Leu Gly Ala Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg 655 660 665 670	2919
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu 675 680 685	2967
gca acc agc gtg c ^a a gcc tgagcggccg ctcgagcatg catctagagg Ala Thr Ser Val Gln Ala 690	3015
gccctattct atagtgtcac ctaatgcta gagctcgctg atcagcctcg actgtgcctt ctagttgcca gccatctgtt gtttgc ^{cc} ctt cccccgtgcc ttccttgacc ctggaagg ^{tg}	3075
ccactcccac tgc ^c tttcc taataaaatg aggaattgc atcgcattgt ctgagtaggt gtcattctat tctgggggtt ggggtggggc aggacagcaa gggggaggat tggaaagaca	3135
atagcaggca tgctggggat gcggtgggct ctatggcttc tgaggcggaa agaacagctg cat ^a atgaa tcggccaacg cg ^c ggggaga ggcggttgc gtattggcg ctctccgct	3195
tcctcgctca ctgactcgct gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg taatacggtt atccacagaa tcagggata acgcaggaaa gaacatgtga	3315
gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cg ^t tgctggc gttttccat aggctccgccc cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac	3375
ccgacaggac tataaagata ccaggcg ^{ttt} cccctggaa gctccctcg ^t ggc ^c tcct gttccgaccc tgccgcttac cggatacc ^t g tccgcctt ^c tcccttcggg aagcgtggcg	3435
gttccgaccc tgccgcttac cggatacc ^t g tccgcctt ^c tcccttcggg aagcgtggcg	3495
gttccgaccc tgccgcttac cggatacc ^t g tccgcctt ^c tcccttcggg aagcgtggcg	3555
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gttccgaccc tgccgcttac cggatacc ^t g tccgcctt ^c tcccttcggg aagcgtggcg	3675
gttccgaccc tgccgcttac cggatacc ^t g tccgcctt ^c tcccttcggg aagcgtggcg	3735

ctttctcaat gctcacgctg taggtatctc agttcggtgt aggtcggtcg ctccaagctg	3795
ggctgtgtgc acgaacccccc cgttcagccc gaccgctgctg ccttatccgg taactatcgt	3855
cttgagtcac acccgtaag acacgactta tcgcccactgg cagcagccac tggtaacagg	3915
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ggctacacta gaaggacagt atttggtatac tgcgcctctgc tgaagccagt taccttcgga	4035
aaaagagttg gtagctctt atccggcaaa caaaccaccg ctggtagccgg tgggtttttt	4095
gtttgcaagc agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt	4155
tctacggggt ctgacgctca gtggAACGAA aactcacgtt aagggatttt ggtcatgaga	4215
ttatcaaaaaa ggatcttcac ctagatcctt ttaaattaaa aatgaagttt taaatcaatc	4275
taaagtatat atgagtaaac ttggctgtac agttaccaat gcttaatcag tgaggcacct	4335
atctcagcga tctgtctatt tcgttcatcc atagttgcct gactccccgt cgttagata	4395
actacgatac gggagggctt accatctggc cccagtgctg caatgataacc gcgagaccca	4455
cgctcaccgg ctccagattt atcagcaata aaccagccag ccggaagggc cgagcgcaga	4515
agtggtcctg caactttatc cgcctccatc cagtttattt attgttgcgg ggaagctaga	4575
gtaagtagtt cggccagttaa tagtttgcgc aacgttggccg ccattgctac aggcacgtg	4635
gtgtcacgct cgtcggttgg tatggcttca ttcaagctccg gttcccaacg atcaaggcga	4695
gttacatgtat ccccatgtt gtcaaaaaaa gcggtagtcccttcgggtcc tccgatcggtt	4755
gtcagaagta agttggccgc agtgttatca ctcattttttt tggcagcact gcataattct	4815
cttactgtca tgccatccgt aagatgttt tctgtgactg gtgagttactc aaccaagtca	4875
ttctgagaat agtgtatgcg gcgaccgagt tgcttttgcc cggcgtcaat acggataat	4935
accgcgccac atagcagaac tttaaaatgt ctcatttgcgaaacgttc ttccgggcga	4995
aaactctcaa ggatcttacc gctgttggaa tccagttcga tgtaaccac tcgtgcaccc	5055
aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa aacaggaagg	5115
caaaatgccg caaaaaagg aataagggcg acacggaaat gttgaataact catacttttc	5175
ctttttcaat attattgttgcg cattttatcgtt ggttattgtc tcatgagccgg atacatattt	5235
gaatgttattt agaaaaataa acaaataagg gttccgcgc aatttccccg aaaagtgcga	5295
cctgacgatc	5304

<210> 22
 <211> 692
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 22

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
20 25 30

Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35 40 45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50 55 60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85 90 95

Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115 120 125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
165 170 175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
195 200 205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
210 215 220

Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
225 230 235 240

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
245 250 255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
260 265 270

Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
290 295 300

Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
305 310 315 320

Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
325 330 335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
340 345 350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
355 360 365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
370 375 380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
385 390 395 400

Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
405 410 415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
435 440 445

Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
450 455 460

Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
465 470 475 480

Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
485 490 495

Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
500 505 510

Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
515 520 525

Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
530 535 540

Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
545 550 555 560

Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
580 585 590

Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
595 600 605

Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
610 615 620

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
660 665 670

Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
675 680 685

Ser Val Gln Ala
690

<210> 23
 <211> 5271
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> CDS
 <222> (910)..(2952)

 <400> 23

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ccgcatagtt	aagccagttat	ctgctccctg	cttgtgtgtt	ggaggtcgct	gagtagtgcg	120
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttagggttag	gcgtttgcg	ctgcttcgcg	atgtacggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacgggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccgcc	tggctgaccg	cccaacgacc	360
cccgccccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggac	tatttacggt	aaactgccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgacacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cgggtttggc	agtacatcaa	tggcgtgga	tagcggttg	660
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ctgcttactg	gcttatcgaa	attaatacga	ctcaactatag	ggagacccaa	gcttggtacc	900
gccggccgcc	atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc					951
	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser					
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Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys						
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aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca						1047
Asn Arg Trp Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr						
35	40	45				
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Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys						
50	55	60				

tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro 65 70 75	1143
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gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg 95 100 105 110	1239
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys 115 120 125	1287
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu 130 135 140	1335
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr 145 150 155	1383
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val 160 165 170	1431
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tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly 195 200 205	1527
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gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile 225 230 235	1623
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr 240 245 250	1671
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu 255 260 265 270	1719
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp 275 280 285	1767
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val 290 295 300	1815

gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val 305 310 315	1863
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly 320 325 330	1911
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp 335 340 345 350	1959
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala 355 360 365	2007
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acc atg aaa ggc gta gaa cgc ctg gcc gtc atg gga gac acc gcc tgg Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp 595 600 605	2727
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile 610 615 620	2775
cat acg gta ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn 625 630 635	2823
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile 640 645 650	2871
aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gta Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val 655 660 665 670	2919
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 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
20 25 30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
35 40 45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
50 55 60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65 70 75 80

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
130 135 140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220

Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225 230 235 240

Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
245 250 255

Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
260 265 270

Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
275 280 285

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305 310 315 320

Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
325 330 335

Gln Glu Asn Trp Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
340 345 350

Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
355 360 365

Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
370 375 380

Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385 390 395 400

Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
405 410 415

His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
420 425 430

Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
450 455 460

His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
465 470 475 480

Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
485 490 495

Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
500 505 510

Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
515 520 525

Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
530 535 540

Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545 550 555 560

Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
565 570 575

Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
580 585 590

Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
595 600 605

Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
610 615 620

Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625 630 635 640

Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
645 650 655

Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
660 665 670

Met Phe Leu Ser Leu Gly Val Gly Ala
675 680

<210> 25
<211> 35

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(35)
<223> POW 454

<400> 25
aaaagaaaaaa gcgctaccac catccaccgg gacag

35

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> CPOW 2417

<400> 26
actgttaccc tcaaccccg actcgccggc gaaaaagaaa a

41

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala
20

<210> 28
<211> 36
<212> DNA

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<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(36)
<223> YF 482

<400> 28
aaaagaaaaa gcgctgtgac cttggtgccg aaaaac 36

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> CYF 2433

<400> 29
acagagatcc tcaaccccgc actcgccggc gaaaaagaaa a 41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> SLE 463

<400> 30
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<210> 31
<211> 40
<212> DNA
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<220>
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<220>
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<222> (1)..(40)
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa

40

<210> 32
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 32

Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
1 5 10 15

Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
20 25 30

Leu Leu Ser Thr Tyr Gln Gly
35

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 33

Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
1 5 10 15

Lys Leu Ser Asn Phe Gln Gly Lys
20

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 34

Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile

1

5

10

15

Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 35

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys
35

<210> 36

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 36

Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15

Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30

Gly Lys

<210> 37

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30

Lys

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 39

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30

Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40
<211> 24
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 42

<211> 5292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 42

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggtagt gcgtttgcg ctgcttcgct atgtacgggc cagatatacg cgttgacatt 240

gattattgac tagtattaa tagtaatcaa ttacgggtc attagttcat agccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360

cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

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gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	951
1 5 10	
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15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	1047
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	1095
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	1143
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	1191
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	1239
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	1287
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	1335
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	1383
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	1431
160 165 170	

aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr 175 180 185 190	1479
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser 195 200 205	1527
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220	1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr 225 230 235	1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys 240 245 250	1671
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc Leu Thr Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro 255 260 265 270	1719
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met 275 280 285	1767
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly 290 295 300	1815
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa Ile Val Thr Cys Ala Met Phe Arg Cys Lys Asn Met Glu Gly Lys 305 310 315	1863
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His 320 325 330	1911
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys 335 340 345 350	1959
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr 355 360 365	2007
ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380	2055
ttc aat gag atg gtg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395	2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410	2151

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aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583
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atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly 595 600 605	2727
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile 610 615 620	2775
gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe 625 630 635	2823
agt ggg gtt tca tgg act atg aaa atc ctc ata gga gtc att atc aca Ser Gly Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr 640 645 650	2871

tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val 655 660 665 670	2919
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actttcacca gcgttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga	5124
ataagggcga cacggaaatg ttgaatactc atactttcc ttttcaata ttattgaagc	5184
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 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct
 <400> 43

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Met Gly Glu His Arg Arg
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245 250 255

Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ile Val
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
625 630 635 640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
645 650 655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
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<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgtttgcg ctgcttcgct atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360
cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggag tatttacggt aaactgccc a cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttggc agtacatcaa tggcgtgga tagcggttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tggagtttgc tttggcacc	720
aaaatcaacg ggactttcca aatgtcgta acaactccgc cccattgacg caaatggcg	780
gtaggcgtgt acgggtggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc	900
gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	951
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	999
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	1047
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	1095
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	1143
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	1191
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	1239
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	1287
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	1335
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	1383
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	1431
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Thr Ala Val Thr Pro Ser Met Thr	1479

175	180	185	190	
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gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220				1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr 225 230 235				1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys 240 245 250				1671
cta acc aac aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc Leu Thr Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro 255 260 265 270				1719
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tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys 335 340 345 350				1959
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ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380				2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395				2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410				2151
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe				2199

415	420	425	430	
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tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg 465 470 475				2343
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aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510				2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525				2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540				2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555				2583
gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Gly Val Glu Pro 560 565 570				2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln 575 580 585 590				2679
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gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe 625 630 635				2823
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu 640 645 650				2871
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu				2919

655	660	665	670	
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct				2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala				
675	680	685		
taattagttt gggcgccgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc				3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg				3084
tttgccttc ccccgtgcct tccttgaccc tggaaagggtc cactcccact gtccttcct				3144
aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg				3204
gggtggggca ggacagcaag ggggaggatt gggaaagacaa tagcaggcat gctggggatg				3264
cggtgtggctc tatggcttct gaggcggaaa gaaccagctg catataatgaa tcggccaacg				3324
cgcggggaga ggcgggttgc gtattggcg ctcttcgct tcctcgctca ctgactcgct				3384
gcgctcggtc gttcggctgc ggcgagcggat atcagctcac tcaaaggcgg taatacggtt				3444
atccacagaa tcagggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc				3504
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cgttcagccc gaccgctgctg ctttatccgg taactatcgt cttgagtcca acccggtaaag				3864
acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt				3924
aggcggtgct acagagttct tgaagtgggt gcctaactac ggctacacta gaagaacagt				3984
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cgcctccatc cagtcttattt attgttgccg ggaagctaga gtaagtagtt cgccagttaa				4584

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gcgaccgagt tgctttgcc cggcgtcaat acggataat accgcgccac atagcagaac	4944
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gctgttggaa tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatctt	5064
tactttcacc agcgttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg	5124
aataagggcg acacggaaat gttgaataact catactcttc cttttcaat attattgaag	5184
catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa	5244
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<210> 45
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct
 <400> 45

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg

100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245 250 255

Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile

340

345

350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe

580

585

590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 46

<211> 5293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 46

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ccgcatagtt aагccагтat ctgctccctg cttgtgtgtt ggагgтcgct gagtagtgcg 120

cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

ttagggtagt gcgtttgcg ctgcttcgct atgtacgggc cагatatacg cgttgacatt 240

gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360

cccgccccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggac tatttacggt aaactgccc a cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540

atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cggtttggc agtacatcaa tggcgtgga tagcggttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tggagtttgc ttggcacc	720
aaaatcaacg ggactttcca aatgtcgta acaactccgc cccattgacg caaatggcg	780
gtaggcgtgt acgggtggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc	900
gccggccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	195	200	205	
gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	210	215	220	1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	225	230	235	1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	240	245	250	1671
cta acc aac aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc Leu Thr Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	255	260	265	1719
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	275	280	285	1767
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly	290	295	300	1815
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa Ile Val Thr Cys Ala Met Phe Arg Cys Lys Asn Met Glu Gly Lys	305	310	315	1863
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	320	325	330	1911
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	335	340	345	1959
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	355	360	365	2007
ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	370	375	380	2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	385	390	395	2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	400	405	410	2151
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	415	420	425	2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt tta gga tcc caa				2247

Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln		
435	440	445
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg		2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met		
450	455	460
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga		2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg		
465	470	475
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga		2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly		
480	485	490
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata		2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile		
495	500	505
510		
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct		2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro		
515	520	525
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att		2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile		
530	535	540
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa		2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu		
545	550	555
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg		2631
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Gly Val Glu Pro		
560	565	570
gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag		2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys		
575	580	585
590		
gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc		2727
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly		
595	600	605
gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata		2775
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile		
610	615	620
gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt		2823
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe		
625	630	635
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc		2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu		
640	645	650
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta		2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu		
655	660	665
670		
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct		2964

Ala	Thr	Gly	Gly	Val	Leu	Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala
				675				680					685	
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ctagatcctt	ttaaaataaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac									4284
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aagatgcttt	tctgtgactg	gtgagtaactc	aaccaagtca	ttctgagaat	agtgtatgcg	4884
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aataagggcg	acacgaaat	gttgaatact	catactcttc	cttttcaat	attattgaag	5184
catttatcag	ggttattgtc	tcatgagcgg	atacatattt	aatgtattt	agaaaaataaa	5244
acaaataggg	gttccgcgca	cattccccg	aaaagtgccca	cctgacgtc		5293

<210> 47
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct
 <400> 47

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
 100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245 250 255

Asn Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
580 585 590

Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
610 615 620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
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Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
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Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
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<400> 61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala
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